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Genetic divergence among accessions of *Manihot* spp.

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ABSTRACT. The aim of this study was to perform a morphological and morphoagronomic analysis of wild *Manihot* species from a Brazilian semiarid region for inclusion in the collection at the Center for Agricultural Sciences, Federal University of Paraíba. To characterize the 55 accessions, 12 quantitative and 18 qualitative descriptors were used. A dissimilarity matrix was generated by Mahalanobis generalized distance (D^2), and clusters were identified by the UPGMA method. It was possible to verify the formation of 8 dissimilar groups based on morphological characters and 5 groups based on morphometric characters, indicating the presence of genetic diversity among accessions. The evaluated morphometric variable with the greatest relative contribution was the length between the central lobe. Based on the dissimilarity matrix, the accessions 16 x 48 were the most genetically distant accessions, followed by 47 x 49. The accessions 4 Monteiro, 16 Soledad, 38 Boa Vista, 3 Pedra Lavrada, 7 Junco, 10 Barra de Santa Rosa, 21 Monteiro, and 39 Junco are the most promising and can be used as parents in breeding programs for this forage species.

Keywords: germplasm bank; agronomic descriptors; morphological descriptors.

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Introducion

The cassava is a naturally occurring plant in the Caatinga, belonging to the family Euphorbiaceae, genus *Manihot*, and is found in several areas of the northeastern semiarid region. It has great persistence to the drought, presents a system of tuberous roots that are very developed and able to accumulate solid reserves and water, and is one of the first species of the Caatinga to develop foliage soon after the beginning of the rainy season. It is used for the maintenance of herds of domestic animals.

The *Manihot* tree species of the northeast region and the herbaceous species of the midwest region have weak barriers to reproductive isolation, which has led to extensive natural hybridization that makes the taxonomy and delineation of these species difficult. The use of morphometric and morphological descriptors can be used as a tool for differentiation through phenotypic characteristics, allowing easy identification and differentiation using a germplasm bank in the field, which is needed due to the high degree of diversity of the species.

One use for the germplasm of the species is to estimate the genetic divergence to predict promising crossings (Krishnamurthy et al., 2013), which can be achieved using morphological and agronomic characters Vieira et al. (2013). Among the phenotypic descriptors, the ones with agronomic importance are most influenced by the environment. Additionally, they help to identify adapted accessions with productive potential.

In view of the above, the objective of this study was to evaluate the genetic diversity and potential of cassava by means of morphometric and morphological characteristic analysis for breeding program inclusion via the germplasm bank.

Material and methods

For the purpose of characterization, 55 accessions of cassava at the reproductive stage of maturation between the end of flowering and the beginning of fruiting were selected for evaluation. Three plants per accession, located in the central line, all belonged to the Germplasm Active Bank (GAB) of the Federal University of Paraíba. The accessions in the BAG came from the Brazilian semiarid region, specifically from the municipalities of Soledade, Juazerinho, Pocinhos, Boa Vista, Sumé, Monteiro, Barra de Santa Rosa, Picuí, Pedra Lavrada, Junco do Seridó, Cubati, Barra de Santana, and along the BR 230 between the municipalities of Boa Vista and Pocinhos (in the State of Paraíba, Brazil) and Taquaritinga do Norte and Santa Cruz do Capibaribe (in the State of Pernambuco, Brazil).

The accessions were spaced with 1.0 m between rows and with 1.0 m between plants, allowing the plants to express full development, avoiding intergenotypic competition, and ensuring vegetative material for analysis as well as duplication for research. For characterization, 12 morphological descriptors and 18 agronomic descriptors were used according to the methodology described by Fukuda, Guevara, Kawuki, and Ferguson (2010).

The quantitative data were submitted to normality adjustment using the equation: $x" = \sqrt{(x + 0.5)}$. The quantitative traits were submitted to analysis of variance, and the means were grouped according to the Scott and Knott (1974) criterion at 5% probability. Then, the dissimilarity was analyzed by generalized Mahalanobis distance (D^2), and clusters were determined by the UPGMA method (Sneath & Sokal, 1973). A bootstrap analysis was performed to verify and provide statistical support to the internal nodes of the dendrograms generated by the UPGMA clustering method using the Genes program (Cruz, 2006). The dendrogram cutoff point and group definition were generated by the hierarchical method described by Mojena (1977).

The validation of the clusters was determined by the cophenetic correlation coefficient (Sokal & Rohlf, 1962). The quantification of the relative contributions of the morphometric characteristics in the genetic divergence was estimated using the methodology proposed by Singh (1981).

Results and discussion

For accessions included in the cut dendrogram, the correlation was approximately 70% based on the morphological characters (Figure 1), and the formation of 8 groups of dissimilarity was observed, indicating diversity between the accessions evaluated; 26 accessions of the 55 evaluated belonged to group VIII. Group VI and group I presented only a single isolated individual, and the group I accession was the most genetically distant when compared to the others. The other groups, although less populous, showed variability among accessions from the same place of origin.

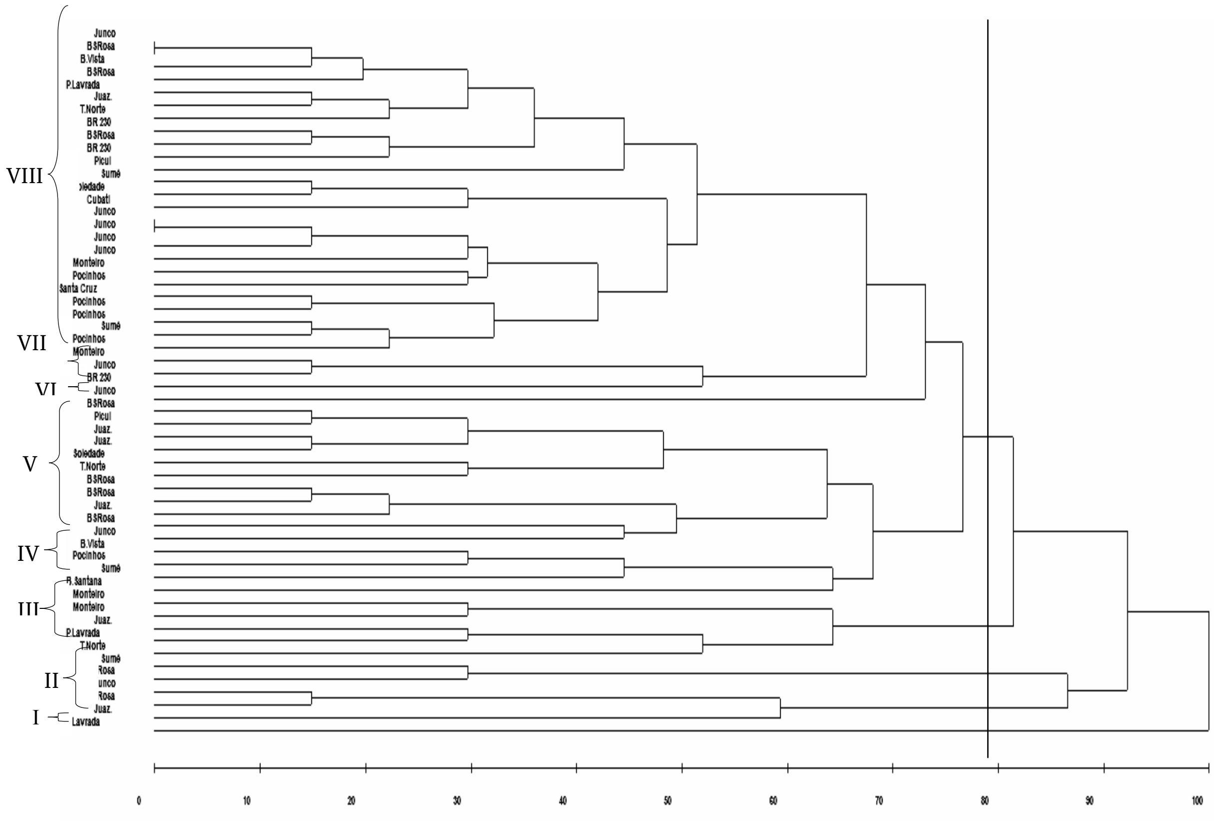

Figure 1. UPGMA dendrogram obtained from the dissimilarity matrix (D2) of the 55 *Manihot* spp. accessions based on 12 morphological descriptors. The cophenetic correlation coefficient was 0.74. The dotted line represents the cutoff point based on the methodology proposed by (Mojena, 1977). Bootstrap values are expressed in percent for 100 repetitions.

Similar results were obtained by Campos et al. (2010) who evaluated the characterization of 53 genotypes of the genus *Manihot* using group analysis based on qualitative and quantitative characteristics, which have been shown to be useful in the study of diversity, serve to support the improvement of and the appropriate use in breeding programs and express the variability present in a germplasm bank based on multiple character evaluations. The least dissimilarity was between accessions Junco 7 and Barra de Santa Rosa 10, and the greatest dissimilarity was between Junco 7 and Pedra Lavrada 3. This genetic distance probably occurs because the accessions originate from opposing localities, making it impossible to exchange genetic material between them.

The cophenetic correlation coefficient obtained for the comparison of the dissimilarity distance matrix and the cophenetic distance matrix was (r = 0.74*) with low distortion and low stress (Table 1), which is considered high and adequate, indicating a good correlation between distance and cluster matrices. Cruz and Carneiro (2006) stated that the higher the cophenetic correlation and the lower the distortion of the cluster, the better the agreement between the original values of dissimilarity and those represented by the dendrogram is, suggesting a good reliability of the data generated.

Table 1. Cophenetic correlation of 12 morphological characters evaluated in 55 accessions of *Manihot* spp.

Cophenetic correlation**	0.74
Degrees of freedom	1483
t-value**	41.83
Distortion (%):	4.79
Stress (%):	21.93

**Significant at $p \leqslant 0.01$.

The percentages of distortions (4.79%) and stress (21.90%) are classified as good according to the Kruskal (1964) scale and show a good fit between the genetic similarity matrix and the graphical representation of the dendrogram (Table 1).

The analysis of the results of the phenotype classes and their respective frequencies affirmed that the accessions belonging to the GAB presented genetic variability. No variability was detected only for the growth character of stipules; all the accessions evaluated presented short stipules, and the other characters had wide variability. These results allow the formation of the hypothesis that these accessions have a broad genetic base, which can be explained by the fact that they are a wild species. According to Asare, Galyuon, Sarfo, and Tetteh (2011), the morphological characteristics are useful for preliminary evaluation since they offer an easy and fast approach to evaluate the extent of diversity.

It was observed that of the 55 evaluated accessions, 28 (50.91%) presented a cylindrical plant type. A dark green leaf color was observed in 90.91%, five lobes were observed in 85.45%, a straight growth habit was observed in 52.73%, and a branching level greater than 5 was observed in 41.82% (Table 2). This wide phenotypic variability is because the genotypes are of different origins. These factors can be taken into account for the choice of accessions in future breeding programs, as they will provide better management qualities, increased photosynthesis, a greater production of leaves and, consequently, more forage production. Silva et al. (2016) observed differences in all the phenotypic characteristics evaluated, reporting the variability of agronomic traits similar to those in this study, proving their efficiency in diversity studies. Vieira, Fialho, Silva, Fukuda, and Faleiro (2008) verified differences in all the quantitative traits, similar to those in this study, which revealed the existence of differences in the agronomic potential of the genotypes and supported the wide variability once accessions from different origins were evaluated.

In the formation of the distinct groups (Figure 2), the variable with the largest number of groups was DMC, comprising six groups with averages varying from 10.73 mm for accession 53 to 36.49 mm for accession 16. This characteristic confers the plant capacity of support and sustentation of the same, mainly because it is a shrub-arbor species.

For plant height (AP), number of axillary buds (NGA), number of floral branches (NRF), and number of senescent leaves (NFS) three groups were formed (a, b and c). Of the 55 accessions evaluated, for the variable plant height, 11 accessions were grouped in group (a) and were considered larger plants with values ranging from 226.30 cm in accession 24 to 155.30 cm in accession 1. Twenty-seven accessions in group b (medium sized) ranged from 147.50 cm in accession 33 and 115.00 cm in accession 43. The smaller plants were in group c with 17 accessions varying between 100.40 cm in accession 34 and 58.60 cm in accession 53.

According to Rós, Hirata, Araújo, and Narita (2011), plant height is an important feature for the adequacy of spacing, for weed competition potential and for the use of branches as propagation material, as taller and densely branched plants generally tend to have a higher potential for foliage production. Taller plants, however, are also more susceptible to bedding, which may hinder the material harvesting process and decrease photosynthetic activity.

The lowest number of groups formed were in the number of flowers (NFlores), number of fruits (NFrutos), and length between leaf lobes (CLBF), with only 2 groups per variable. The number of flowers and fruits should be taken into account when a cross between an accession and propagated specimen of the same species is desired by means of seeds.

Table 2. Characteristics of the phenotype classes (morphology) evaluated and frequency of accessions in each class.

Feature	Phenotypic Classes	Number of accessions	Frequency of accessions (%)
Type of plant	1-Compact	1	1.82
	2- Open	14	25.45
	3- Sun Guard	12	21.82
	4- Cylindrical	28	50.91
Apical leaf color	1- Light green	4	7.27
	2- Dark green	50	90.91
	3- Green purple	1	1.82
Central lobe shape	1- Ovoid	3	5.45
	2- Elliptical-Lanceolate	3	5.45
	3-Obovate- Lanceolate	46	83.64
	4- Lanceolate	3	5.45
Rib color	1- Green	42	76.36
	2- Green with red in less than half of the lobe	13	23.64
Number of lobes	1- Three Lobes	4	7.27
	2- Five Lobes	47	85.45
	3- Seven lobes	3	5.45
	4- Nine Lobes	1	1.82
Growth habit	1- Straight	29	52.73
	2-Zig-zag	26	47.27
Color of terminal branches on adult plants	1- Green	28	50.91
	2- Green purple	26	47.27
	3- Purple	1	1.82
Branching levels	1-One	5	9.09
	2-Two	9	16.36
	3-Tree	6	10.91
	4- For	12	21.82
	5-≥ Five	23	41.82
Position of the petiole	1- inclined	29	52.73
	2- horizontal	26	47.27
Lengths of stipules	1- Short	55	100.00
	2- Long	0	0.00
Leaf lobe sinuosity	1- Smooth	38	69.09
	2- Winding	17	30.91
Petiole color of green leaf	1- Reddish Green	42	76.36
	2- Red	9	16.36
	3- Purple	4	7.27

For the number of branches (NR), number of leaves (NFs), diameter of the base of the leaf petiole (DBPF), mean leaf petiole diameter (DMPF), central lobe length (CLC), and upper lobe width LSLC), 4 groups were formed. For leaf petiole length (CPF), upper leaf petiole diameter (DSPF), and length between leaf median lobes (CLMF), 5 groups were formed. These characteristics are important in choosing the parents because, when used as fodder, they may provide a greater yield of dry matter.

The greatest values found for length between the median lobes of the leaves were those belonging to group a, ranging from 28.30 cm in accession 3 and 24.15 cm in accession 30, and this character could be selected from a possible parent. Ledo et al. (2011) stated that the relationship between the length and width of the central lobe as well as the width of the central lobe influence the photosynthetic rate and, consequently, leaf mass production.

The median width of the central lobe (LMLC) consisted of 8 distinct groups with higher values, ranging from 16.00 cm in accession 15 and 18.50 in for accession 18, both of which belonged to group a (4 accessions). The lowest values were found in accessions 48 and 53 at 3.80 and 3.30 cm, respectively. Narrow leaf lobes allow less shading between the leaves of the same plant, which allows a better distribution and use of solar rays for photosynthesis.

Acesso	AP (cm)	DCM (mm)	NGA	NR	N Leaf	NFL	NRFL	N fruit	NFS	CPF (cm)	DBPF (mm)	DMPF (cm)	DSPF (mm)	CLC (cm)	LMLC (cm)	LSLC (cm)	CLMF (cm)	CLBF (cm)
1	155,33a	32.37b	90b	11b	199a	2b	5b	28a	25a	17.50b	7.58a	4.78b	5.12b	18.83a	8.50e	6.60a	23.00a	21.80a
2	133,66b	26.90c	55b	11b	104b	0b	0c	0b	12a	16.20b	4.5b	3.64c	4.82c	15.66b	5.83f	3.50d	21.45b	19.30
3	115,2b	16.81e	22b	1d	20d	0b	1c	0b	1c	17.50b	6.28a	5.89a	7.89a	19.50a	9.07d	8.60a	28.30a	27.80a
4	176,1a	35.17a	198a	16a	142a	0b	0c	22a	33a	8.5e	2.83d	2.29d	2.81e	11.50c	6.50f	4.30c	17.80c	15.65b
5	111b	17.65e	29b	2d	32d	0b	0c	3b	7c	17.00b	5.29b	3.55c	4.33c	14.33b	6.00f	4.80c	19.30b	17.15b
6	79.00c	16.52e	10c	1d	31d	0b	0c	1b	0c	12.30d	3.32d	2.85d	3.89d	12.23c	4.25h	4.30c	13.10d	15.65b
7	153.00a	20.66d	27a	4c	54c	0b	0c	12a	15b	17.40b	5.60a	4.26b	4.82c	17.30a	7.50e	5.30b	19.00b	17.10b
8	146.00b	20,81d	21b	5c	72b	0b	0c	1b	3c	17.60b	3.79c	3.62c	4.52c	17.83a	7.50e	5.55b	21.50b	21.40a
9	143.00b	20.82d	28c	2d	12d	0b	0c	4b	1c	14.10c	4.50b	3.38c	4.12d	13.00c	7.15e	5.60b	12.90d	20.90a
10	108.50c	24.52c	100a	8b	112b	0b	0c	18a	24a	10.10d	3.69c	4.09c	3.20e	10.50d	4.75g	3.90d	12.75d	13.95b
11	165.30a	28.54c	94b	9b	54c	0b	0c	24a	13b	13.80c	4.58b	3.61c	4.48c	14.23b	7.05e	5.90b	16.25c	20.50a
12	144.30b	25.53c	42b	11b	81b	0b	0c	7b	22a	10.10d	3.80c	3.08d	3.39d	16.33b	12.15b	5.80b	4.80e	15.65b
13	121.30b	19.55d	36b	5c	54c	0b	0c	10b	2c	10.00d	4.62b	3.50c	4.15d	13.83c	12.50b	6.20b	4.65e	10.00b
14	150.00b	28.41c	35b	6b	72b	0b	2c	20a	0c	6.50e	2.86d	2.55d	2.33e	13.00c	11.10c	5.60b	4.00e	7.60b
15	117.30b	20.64d	37b	6b	38c	0b	0c	1b	6c	15.80c	6.21a	3.80c	4.85c	19.07a	16.00a	7.05a	5.60e	20.90a
16	173.00a	36.49a	138a	23a	188a	26a	9a	0b	22a	18.00b	4.74b	3.01d	3.38d	18.83a	15.50a	5.25b	3.50e	19.25a
17	143.30b	26.73c	36b	8b	39c	0b	0c	4b	8b	12.80c	4.74b	3.83c	4.61c	19.33a	14.50a	7.00a	5.90e	21.50a
18	169.30a	25.65c	48a	10b	62c	0b	0c	5b	12b	12.30c	5.02b	3.64c	4.82c	18.50a	14.50a	7.00a	5.30e	21.00a
19	150.00b	26.47c	41b	5c	62c	0b	0c	26a	1c	12.60d	5.44a	3.69c	3.82d	12.17c	12.00b	7.00a	5.50e	21.00a
20	127.60b	21.02d	18b	1d	12d	0b	2c	8b	2c	13.30c	3.95c	3.58c	3.98d	10.33d	12.00b	6.10b	5.30e	11.55a
21	144.30b	23.44c	16b	4c	43c	0b	0c	2b	4c	16.60b	4.27c	3.79c	4.62c	17.66a	12.50b	6.65a	5.50e	16.15b
22	63.50c	19.53c	8c	1d	7d	0b	0c	1b	3c	9.00d	3.90c	2.92d	2.55e	13.66c	11.20c	5.10b	3.60e	16.00b
23	77.60c	17.84e	16c	1d	27d	0b	0c	1b	5c	10.10d	3.19d	2.89d	3.05e	12.16c	10.30c	4.50c	4.00e	14.00b
24	226.30a	29.76b	54a	11b	106b	0b	0c	7b	8b	16;00c	3.58c	3.27c	3.85d	16.33b	11.60b	6.65a	5.15e	19.30a
25	118.00b	20.87d	17b	6b	41c	0b	0c	3b	11b	10.60d	4.12c	3.08d	3.39d	12.88c	11.30c	5.50b	4.30e	16.15b
26	76.60c	18.34d	37c	4c	32c	0b	0c	1b	2c	6;80e	3.05d	2,17d	2.21e	11.10c	9.30d	4.65c	3.80e	13.65b
27	76.60c	16.19e	17c	1d	23d	0b	0c	0b	3c	13.70c	3.62c	3.73d	2.94e	15.83b	14.00b	4.80c	4.00e	15.50b
28	164.00	25.25c	39a	9b	120b	0b	0c	2b	8b	15.10c	5.84a	3.32c	4.03d	19.83a	14.00b	5.80b	5.15e	18.50a
29	142.60b	18.86d	20b	3d	37c	0b	1c	4b	2c	15.50c	4.83b	4.44c	4.13d	16.17b	12.00b	5.10b	4.80e	15.60b
30	145.30b	28.50c	22b	5c	74b	0b	0c	0b	0c	24.80a	5.42a	3.99b	9.24a	16.83b	8.40e	7.00a	24.15a	26.00a
31	78.00a	30.23b	41a	8b	72b	0b	0c	15a	3c	13.00c	4.63b	2.97c	4.27c	18.33a	12.50b	5.10b	4.80e	19.80a
32	98.60c	19.60d	6c	1d	25d	0b	0c	0b	0c	9.20d	3.99c	2.95d	5.27b	9.8d	5.00g	3.50d	13.60d	11.25b
33	147.50b	22.52d	16b	9b	52c	0b	0c	0b	0c	19.80b	3.61c	3.35d	5.10b	13.13c	5.90f	5.20b	17.85c	17.45a
34	100.40c	17.33e	7c	3c	14d	0b	0c	3b	3c	11.80d	4.22c	3.51c	3.78d	12.50c	5.70f	4.15c	13.80d	18.15a
35	168.70a	27.25c	134a	15a	163a	0b	1c	15a	9b	15.80c	6.07a	3.96c	4.01d	15.87b	6.20f	4.50c	22.00b	19.80a
36	121.30b	17.60e	35b	6b	37c	0b	0c	2b	4c	9.90d	4.89b	2.53c	4.38c	12.50c	5.30g	3.50d	16.15c	16.30b
37	77.30c	14.65e	6c	5c	44c	0b	0c	2b	3c	9.80d	4.29c	2.28d	2.73e	9.5d	5.00g	4.50c	12.80d	15.30b
38	161.80a	29.20b	86a	10b	194a	0b	0c	40a	2c	9.50d	3.99c	4.12d	2.94e	11.5c	5.50g	4.50c	14.65d	15.50b
39	136.00b	20.53d	39b	5c	57c	0b	1c	3b	2c	12.10d	5.77a	4.03c	5.68b	13.67c	6.80e	5.50b	16.30c	19.15a
40	142.00b	21.70d	31b	6b	60c	0b	0c	16a	5c	16.30b	5.54a	3.53c	4.28c	18.83a	7.30e	4.85c	24.50a	24.65a
41	126.00b	18.62d	19b	5c	49c	0b	0c	7b	2c	13.90c	4.71b	3.60c	4.10d	15.67b	5.20g	3.30d	17.50c	19.00a
42	100.50c	19.53d	7c	3c	42c	0b	0c	0b	2c	16.50b	4.55b	3.05c	4.45c	15.33b	5.00g	4.05c	22.15b	14.80b
43	115.00b	21.83d	35b	4c	24d	0b	1c	7b	1c	8.00e	3.92c	4.45d	3.43d	9.67d	3.80h	3.30d	14.15d	13.30b
44	117.30b	23.82c	31b	4c	67b	0b	0c	1b	16b	21.30a	5.46a	3.85b	4.81c	16.83b	8.20d	6.30a	26.15a	13.00b
45	134.00b	21.51d	24b	4c	73b	0b	0c	29a	1c	13.00c	5.46a	3.61c	4.89c	14.50b	5.80f	5.15b	17.30c	12.65b
46	63.40c	18.30d	8c	1d	17d	0b	0c	0b	0c	18.30b	4.09c	3.65c	6.25b	14.37b	6.20f	5.55b	21.65b	24.50a
47	88.50c	16.52e	10c	2d	38c	0b	0c	0b	0c	16.40b	4.28c	2.20c	5.78b	11.83c	5.30g	5.40b	20.30b	16.00b
48	64.00c	18.60d	8c	1d	17d	0b	0c	0b	0c	6.80e	2.68d	3.46d	3.48d	7.67d	3.50h	3.05d	10.80d	9.40b
49	88.00c	16.52e	8c	2d	41c	0b	0c	0b	0c	13.80c	3.99c	2.80c	4.82c	11.47c	6.25f	5.65b	17.23c	15.60b
50	82.30c	16.75e	8c	1d	12d	0b	0c	0b	0c	10.80d	3.05d	3.36d	3.95d	10.37d	4.10h	3.80d	16.10c	15.40b
51	112.30b	16.56e	17b	1d	19d	0b	0c	0b	0c	15.50c	3.91c	2.91c	5.28b	11.88c	5.05g	5.60b	19.50b	14.45b
52	118.00b	16.34d	24b	3c	44c	0b	0c	4b	0c	14.50c	4.22c	2.43d	5.27b	10.60d	4.60g	4.70c	14.10d	17.10a
53	58.60c	10.73f	3c	2d	25d	1b	1c	0b	0c	13.50c	2.53d	3.71d	3.60d	7.80d	3.30h	3.60d	12.60d	9.50b
54	80.60c	20.77d	4c	2d	35c	1b	1c	3b	0c	14.70c	4.56b	2.79c	5.78b	10.27d	3.60h	6.00b	19.35b	11.15b
55	84.00c	18.73d	10c	2d	45c	0b	0c	3b	1c	13.10c	4.04c	2.81d	2.99e	10.30d	5.00g	4.70c	11.20d	16.00b

Figure 2. The averages of 18 morphometric characters evaluated in 55 accessions (*Manihot* spp.) AP = plant height; NGA = number of axillary buds; DMC = mean stem diameter (mm); NR = number of branches; NFolhas = number of leaves; NFL number of flowers, NRFL- number of floral bouquets; NFR = number of fruits; NFS = number of senescent leaves; CPF = leaf petiole length (cm); DBPF = diameter of the leaf petiole base (mm); DMPF = mean leaf petiole diameter (mm); DSPF = upper leaf petiole diameter (mm); CLC = central lobe length (cm); LMLC = median lobe width (cm); LSLC = upper lobe width (cm); CLMF = length between the leaf lobes (cm); CLBF = length between the leaf lobes. *Means followed by the same letter in the columns do not differ statistically from the genetic group by the Scott-Knott test at 5%.

It was possible to detect differences in the variation, with the variable length between the central lobes representing 19.17%. It is a characteristic of great importance in regard to the use of the species as forage since the size of leaf can infer a greater percentage of leaf mass (Table 3).

Following the criterion of relevance, the number of axillary buds contributed 19.06%, plant height contributed 16.86% and the median central lobe width contributed 13.44%. The number of productive buds has great importance for branching and thus can contribute to the increase of productivity of greens and dry mass, which are the parts of the plant most used in animal feed.

The variables base diameter and mean diameter of the leaf petiole can be ruled out in future breeding studies since they contributed only 0.66 and 0.44%, respectively, in the study of the diversity among the accessions.

The matrix of genetic dissimilarity generated from morphometric data is shown in (Figure 3), showing the proximity and distance between the accessions evaluated. The most similar pair of accessions were 47 x 49 (1.464), which could be discarded in the parental choice if used only for genetic proximity, reducing its contribution to the breeding program. The most dissimilar pair of accessions among all the accessions were 16 x 48 (209.592), which makes them the most suitable to be used as parents of *Manihot* spp. for the genetic mapping of genes of interest.

Table 3. Relative contribution of traits to diversity (Singh, 1981) based on the generalized Mahalanobis distance.

Variable	Value in %
Length between the central lobes (cm)	19.17
Number of axillary buds	19.06
Plant height	16.86
Median lobe width (cm)	13.44
Number of flowers	8.89
Upper diameter of leaf petiole (mm)	3.93
Number of sheets	3.01
Mean diameter of stem (mm)	2.51
Length of the medial lobe (cm)	2.20
Length of leaf petiole (cm)	2.19
Number of branches flower	2.12
Number of fruits	1.77
Number of senescent leaves	1.44
Length between basal leaf lobes (cm)	0.81
Upper lobe center width (cm)	0.79
Number of branches	0.68
Diameter of leaf petiole base (mm)	0.66
Mean diameter of leaf petiole (mm)	0.44

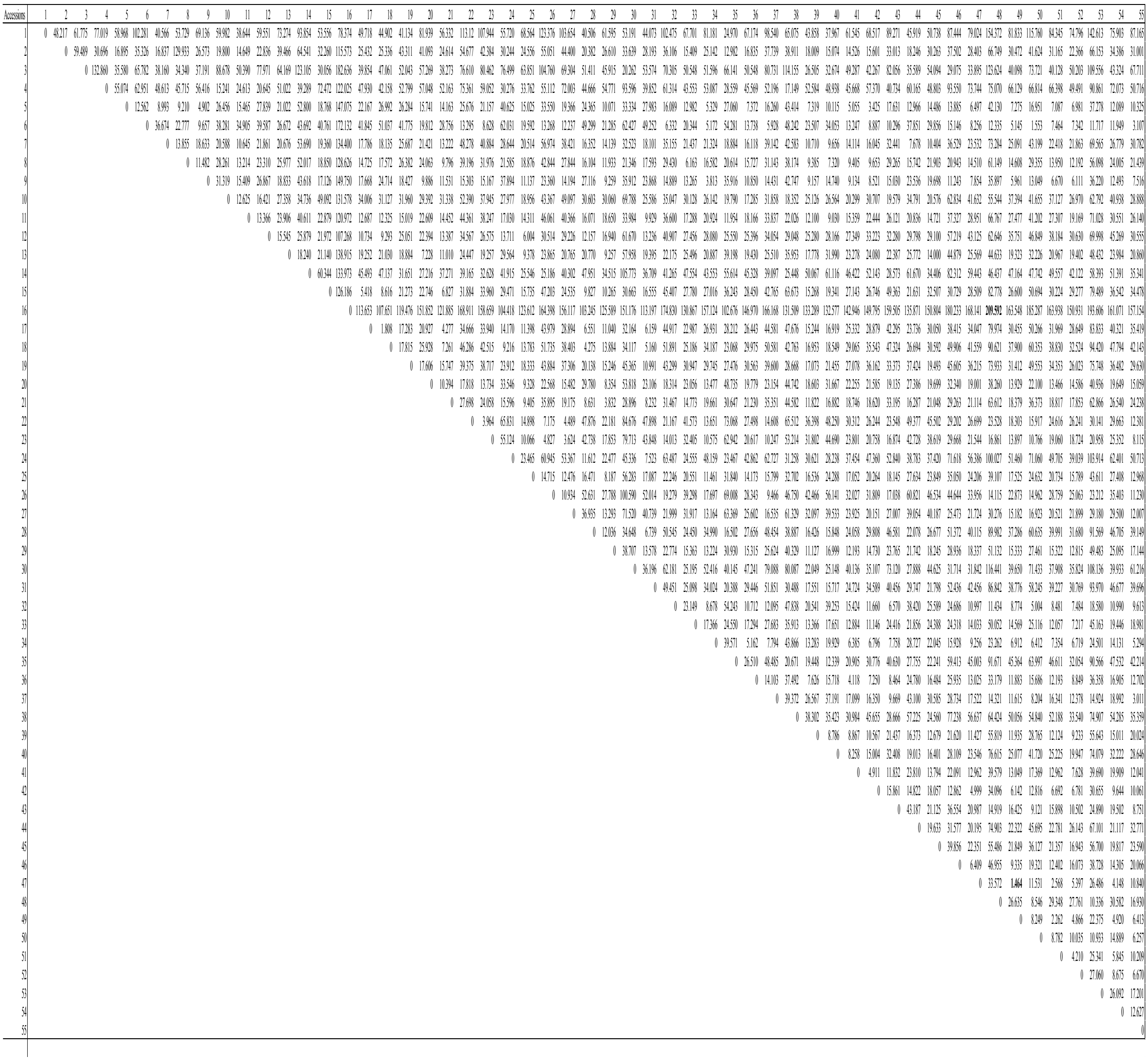

Figure 3. Matrix of genetic dissimilarity obtained by the generalized Mahalanobis distance based on the morphometric characters of the 55 accessions of *Manihot* ssp. Areia, Paraíba State, Brazil.

The cluster produced by the UPGMA method was subjected to a cut of approximately 79%, allowing the formation of 5 well-distributed, distinct groups (Figure 4). The divergence between and among the groups, including individuals from the same locality belonging to different genetic groups presenting different characteristics, can be used for future breeding work. Bootstrap values with 89 and 92% dissimilarity provided reliability in the formation of dendrogram branches. According to Cruz (2006), these values represent a true significant junction, inferring the consistency and adaptation of the dendrogram to represent dissimilarity between the accessions.

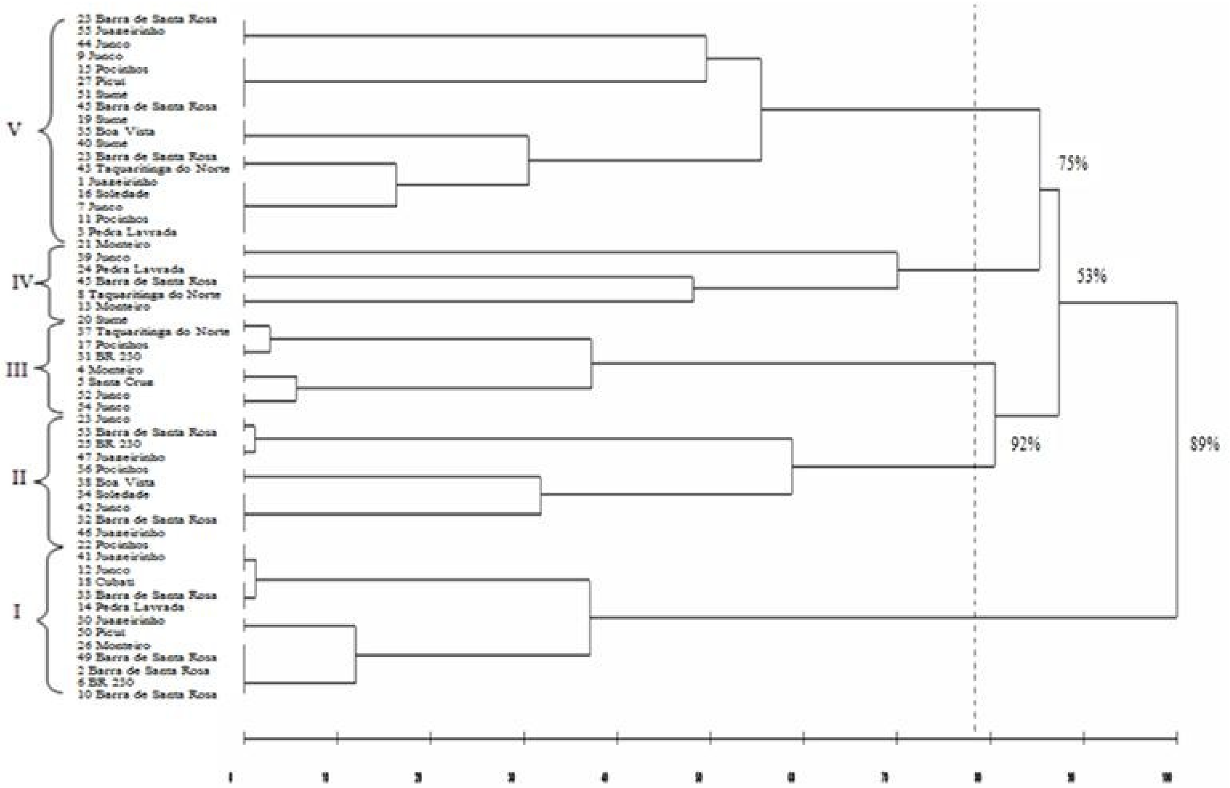

Figure 4. UPGMA dendrogram obtained from the dissimilarity matrix (D2) of the 55 *Manihot* spp. accessions based on 18 agronomic characters. The cophenetic correlation coefficient was 0.85. The dotted line represents the cutoff point based on the methodology proposed by (Mojena, 1977). Bootstrap values for 100 repetitions are expressed in percent.

Campos et al. (2010) evaluated the genetic divergence among 53 accessions of the *Manihot* genus using 28 morphoagronomic descriptors and verified the formation of ten genetic groups. They concluded that the genus presents a high degree of variability, being therefore very diversified, and demonstrated that these variables present high variability when analyzing the species of the *Manihot* genus.

Araujo, Ledo, Martins, and Santos (2012) evaluated 10 quantitative and 22 qualitative characteristics similar to those used in this study in 145 accessions of two wild species of *Manihot* and verified the formation of 3 groups of dissimilar genotypes by the UPGMA method. These results showed the presence of genetic diversity among the evaluated genotypes, demonstrating the efficacy of the morphological descriptors for the characterization and determination of the genetic diversity.

The cophenetic correlation coefficient (Table 4) was 0.85%, indicating a high correlation between distance and cluster matrices. The higher the correlation value, the less distortion caused by the grouping exists (Manly, 2019). The percentages of distortions (11.42%) and stress (23.80%), according to the Kruskal (1964) scale, are classified as good, showing a good fit between the genetic similarity matrix and the graphical representation of the dendrogram.

Table 4. Cophenetic correlation of 18 morphoagronomic characters evaluated in the 55 accessions (*Manihot* spp.).

Cophenetic correlation**	0.85
Degrees of freedom	1483
t-value**	61.68
Distortion (%)	11.42
Stress (%)	23.80

**Significant at $p \leq 0.01$.

Conclusion

In this work, it was observed that there was genetic variability between the accessions evaluated based on the morphological and morphometric characteristics. These characteristics should be considered in the choice of the potential parents for a genetic improvement programs and for forage purposes.

The accessions 4 Monteiro, 16 Soledade, 38 Boa Vista, 3 Pedra Lavrada, 7 Junco, 10 Bar of Santa Rosa, 21 Monteiro, and 39 Junco are the most promising parental accessions.

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